08/813 323

DEPARTMENT OF COMMERCE
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		FIRST NAMED APPLICANT	
SERIAL NUMBER 1 3	FILING DATED 3/10/97	BALTIMORE	ATTORNEY DOCKET NO.
			D 50659/JPW/JM

JOHN P WHITE
COOPER AND DUNHAM
1185 AVENUE OF THE AMERICAS
NEW YORK NY 10036

18M1/1112

RECEIVED
COOPER & DUNHAM

NOV 14 1997

DOCKET CLERK

EXAMINER	
EYLER, Y Yvonne Eyler, Ph.D.	
ART UNIT	PAPER NUMBER
1806	1806

DATE MAILED: 11/12/97

12/12/97

Commissioner of Patents

Please find below a communication from the EXAMINER in charge of this application

The communication filed on 8/04/97 is not fully responsive to the communication mailed 5/30/97 for the reasons set forth on the attached Notice to Comply with the Sequence Rules or CRF Diskette Problem Report.

Since the response appears to be <u>bona fide</u>, but through an apparent oversight or inadvertence failed to provide a complete response, Applicant is required to complete the response within a time limit of one (1) month from the date of this letter or within the time remaining in the response period of the communication mailed 5/30/97, whichever is the longer. 37 C.F.R. 1.135 (c).

Any inquiry concerning this communication should be directed to Examiner Yvonne Eyler, Art Unit 1806, whose telephone number is (703) 308-6564.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Any questions regarding compliance with the sequence rules requirements specifically should be directed to the departments listed at the bottom of the Notice to Comply.

NO EXTENSION OF TIME LIMIT MAY BE GRANTED UNDER EITHER 37 C.F.R. 1.136 (a) OR (b), BUT THE STATUTORY PERIOD FOR RESPONSE SET IN THE COMMUNICATION MAILED 6/7/96 MAY BE EXTENDED UP TO A MAXIMUM OF SIX (6) MONTHS UNDER 37 C.F.R. 1.136.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Yvonne Eyler, Ph.D. whose telephone number is (703) 308-6564. The examiner can normally be reached on Monday through Friday from 830am to 630pm.
If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lila Feisee, can be reached on (703) 308-2731. The fax phone number for this Group is (703) 305-3014 or (703) 308-4242.
Communications via Internet e-mail regarding this application, other than those under 35 U.S.C. 132 or which otherwise require a signature, may be used by the applicant and should be addressed to [lila.feisee@uspto.gov].
All Internet e-mail communications will be made of record in the application file. PTO employees do not engage in Internet communications where there exists a possibility that sensitive information could be

identified or exchanged unless the record includes a properly signed express waiver of the confiden :lity requirements of 35 U.S.C.   ?.   This is more clearly set forth in the Interim Internet Usage Policy published in the Official Gazette of the Patent and Trademark on February 25, 1997 at 1195 OG 89.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

11/10/97
Yvonne Eyler

LILA FEISEE
SUPERVISORY PATENT EXAMINER
GROUP 1800

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29 May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."

☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

☐ 7.

Other: _____

Applicant must provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.

The Scientific and Technical Information Center (STIC) experienc d a problem when pr cessing the following CRF diskette:

Application Serial Number: _08/ 813 323_

Filing Date: _3/10/97_

Classification: _530_

Date Processed by STIC: _9/10/97_

Point-of-Contact/Telephone No.: **Arti Shah   703 - 308 - 4212**

Nature of Problem:

The diskette was:

___ Damaged

___ Unreadable

___ Blank (no files present on diskette)

___ Contained an empty file (filename present, but no bytes in file)

___ A computer virus was detected on the diskette. The STIC will not process the diskette through the Data Capture System.

   Name of virus: _____

_✓_ The Sequence Listing was not saved in ASCII (DOS) text.

___ The diskette contained an error that disrupted normal processing:

_____
_____
_____

SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: Baltimore, David
                Cheng, Genhong
                Cleary, Aileen
                Lederman, Seth
                Ye, Zheng-sheng

  (ii) TITLE OF INVENTION: TRUNCATED CRAF1 INHIBITS CD40 SIGNALING

 (iii) NUMBER OF SEQUENCES: 5

  (iv) CORRESPONDENCE ADDRESS:
      (A) ADDRESSEE: Cooper & Dunham, LLP
      (B) STREET: 1185 Avenue of the Americas
      (C) CITY: New York
      (D) STATE: New York
      (E) COUNTRY: USA
      (F) ZIP: 10036

   (v) COMPUTER READABLE FORM:
      (A) MEDIUM TYPE: Floppy disk
      (B) COMPUTER: IBM PC compatible
      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
      (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

  (vi) CURRENT APPLICATION DATA:
      (A) APPLICATION NUMBER:
      (B) FILING DATE:
      (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
      (A) NAME: White, John P
      (B) REGISTRATION NUMBER: 28,678
      (C) REFERENCE/DOCKET NUMBER: 50659

  (ix) TELECOMMUNICATION INFORMATION:
      (A) TELEPHONE: (212) 278-0400
      (B) TELEFAX: (212) 391-0525

(2) INFORMATION FOR SEQ ID NO:1:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 566 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: peptide

  (ix) FEATURE:
      (A) NAME/KEY: Peptide
      (B) LOCATION: 1..566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Met Glu Ser Ser Lys Lys Met Asp Ala Ala Gly Thr Leu Gln Pro Asn
1               5                   10                  15

Pro Pro Leu Lys Leu Gln Pro Asp Arg Gly Ala Gly Ser Val Leu Val
            20                  25                  30

Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu Asp
        35                  40                  45

Lys Tyr Lys Cys Glu Lys Cys Arg Leu Val Leu Cys Asn Pro Lys Gln
        50                  55                  60

Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu Leu
65                  70                  75                  80

Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Ile Lys
                85                  90                  95

Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala Leu
            100                 105                 110

Gln Val Tyr Cys Arg Asn Glu Gly Arg Gly Cys Ala Glu Gln Leu Thr
        115                 120                 125

Leu Gly His Leu Leu Val His Leu Lys Asn Glu Cys Gln Phe Glu Glu
    130                 135                 140

Leu Pro Cys Leu Arg Ala Asp Cys Lys Glu Lys Val Leu Arg Lys Asp
145                 150                 155                 160

Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr Cys
            165                 170                 175

Ser His Cys Lys Ser Gln Val Pro Met Ile Lys Leu Gln Lys His Glu
        180                 185                 190

Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys Ser
        195                 200                 205

Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys
    210                 215                 220

Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe
225                 230                 235                 240

Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val
            245                 250                 255

Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys
        260                 265                 270

Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile Gln
    275                 280                 285
```

```
Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln
        290                 295                 300

Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg
    305                 310                 315                 320

Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile
                325                 330                 335

Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser
            340                 345                 350

Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys
        355                 360                 365

Ser Ala Gly Gln Ala Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu
    370                 375                 380

Ser Arg His Asp Gln Thr Leu Ser Val His Asp Ile Arg Leu Ala Asp
385                 390                 395                 400

Met Asp Leu Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val
                405                 410                 415

Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val
            420                 425                 430

Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr
        435                 440                 445

Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met
    450                 455                 460

Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu
465                 470                 475                 480

Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met
                485                 490                 495

Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys
            500                 505                 510

Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn
        515                 520                 525

Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn
    530                 535                 540

Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp
545                 550                 555                 560

Thr Ser Asp Leu Pro Asp
                565
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 568 amino acids

```
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide


    (ix) FEATURE:
          (A) NAME/KEY: Peptide
          (B) LOCATION: 1..568


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn
1               5                   10                  15

Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe
            20                  25                  30

Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
        35                  40                  45

Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
    50                  55                  60

Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu
65                  70                  75                      80

Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
            85                  90                  95

Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
        100                 105                 110

Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
        115                 120                 125

Thr Leu Gly His Leu Leu Val His Leu Lys Asn Asp Cys His Phe Glu
    130                 135                 140

Glu Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys
145                 150                 155                 160

Asp Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr
            165                 170                 175

Cys Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His
            180                 185                 190

Glu Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys
        195                 200                 205

Ser Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu
    210                 215                 220

Cys Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val
225                 230                 235                 240
```

```
Phe Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala
                245                     250                 255

Val Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys
                260                 265                 270

Lys Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile
                275                 280                 285

Gln Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg
        290                 295                 300

Gln Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln
305                     310                 315                 320

Arg Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu
                325                 330                 335

Ile Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser
                340                 345                 350

Ser Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp
            355                 360                 365

Lys Ser Ala Gly Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln
        370                 375                 380

Leu Ser Arg His Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala
385                     390                 395                 400

Asp Met Asp Leu Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly
                405                 410                     415

Val Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala
                420                 425                 430

Val Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly
            435                 440                 445

Tyr Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly
    450                 455                 460

Met Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly
465                 470                 475                 480

Glu Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu
                485                 490                 495

Met Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe
            500                 505                 510

Lys Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met
            515                 520                 525

Asn Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu
        530                 535                 540
```

Asn Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val
    545   550   555   560

Asp Thr Ser Asp Leu Pro Asp Pro
         565

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2359 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
GGCGGCGGAG GATGCGCGCG GCGCCTGAGC CGGCCGAACG GGCGGCCTCG GGGTACAGGG      60

TCCCCATTAC TTGAAGGATA AGGCTGGCAC GGCTCCGACG TCTGTGTGGA AGCTTCTCCC     120

TCCCTTCTGA GCTTCTCTAG ACTCCTTACA GCGCACGGCA CAGAATTTCA GTTTCCTAAG     180

ATGGAGTCAA GCAAAAAGAT GGATGCTGCT GCACACTGC AGCCTAACCC ACCCCTAAAG     240

CTGCAGCCTG ATCGCGGCGC AGGGTCCGTG CTCGTGCCGG AGCAAGGAGG CTACAAGGAG     300

AAGTTTGTGA AGACGGTGGA AGACAAGTAC AAGTGCGAGA AGTGCCGCCT GGTGCTGTGC     360

AACCCGAAGC AGACGGAGTG TGGCCACCGG TTCTGCGAGA GCTGCATGGC CGCCCTGCTG     420

AGCTCCTCCA GTCCAAAATG CACAGCGTGC CAAGAAAGCA TCATCAAAGA CAAGGTGTTT     480

AAGGATAATT GCTGCAAGAG AGAGATTCTG GCCCTTCAGG TCTACTGTCG GAATGAAGGC     540

AGAGGTTGTG CGGAGCAGCT GACTCTGGGA CATCTGCTGG TGCACCTAAA AAATGAATGT     600

CAGTTTGAGG AACTTCCCTG TCTGCGTGCC GACTGCAAAG AAAAGTACT GAGAAAAGAC      660

TTGCGGGATC ACGTGGAAAA GGCCTGTAAA TACCGCGAGG CCACGTGCAG TCACTGCAAG     720

AGCCAAGTGC CCATGATCAA ACTGCAGAAA CATGAAGACA CAGATTGTCC CTGTGTGGTG     780

GTATCCTGCC CTCACAAGTG CAGCGTTCAG ACTCTTCTAA GGAGTGAGTT GAGTGCACAC     840

TTGTCCGAGT GTGTCAATGC CCCCAGCACC TGTAGTTTTA AGCGCTATGG CTGCGTTTTT     900

CAGGGTACAA ACCAGCAGAT CAAGGCCCAT GAGGCCAGCT CCGCGGTACA GCACGTGAAC     960

CTGCTGAAGG AGTGGAGCAA CTCCCTGGAG AAGAAGGTTT CCCTGCTGCA GAATGAAAGT    1020

GTTGAGAAAA ACAAGAGCAT CCAAAGCCTG CACAACCAGA TCTGCAGCTT TGAGATCGAG    1080

ATTGAGAGGC AGAAGGAGAT GCTCCGAAAC AACGAGTCCA AGATCCTTCA CCTGCAGCGG    1140
```

GTAATCGACA GCCAAGCAGA GAAACTGAAA GAACTGGACA AGGAGATCCG TCCCTTCCGG   1200

CAGAACTGGG AGGAAGCGGA CAGCATGAAG AGCAGTGTGG AGTCCCTCCA GAACCGAGTG   1260

ACTGAGCTGG AGAGCGTAGA CAAAAGTGCG GGGCAGGCGG CTCGCAACAC AGGCTTGCTG   1320

GAGTCCCAGC TGAGCCGGCA TGACCAGACG TTGAGTGTTC ATGACATCCG CTTGGCCGAC   1380

ATGGACCTGC GGTTCCAGGT CCTCGAGACC GCCAGCTACA ACGGGGTGCT GATCTGGAAG   1440

ATCCGTGACT ACAAGCGCCG GAAGCAGGAG GCCGTCATGG GGAAGACCCT GTCTCTCTAC   1500

AGCCAGCCTT TCTACACAGG TTATTTTGGC TATAAGATGT GTGCCAGGGT CTACCTGAAT   1560

GGGGACGGAA TGGGGAAAGG GACACACTTG TCGCTGTTTT TTGTCATTAT GCGTGGAGAA   1620

TATGATGCTC TGTTGCCATG GCCGTTCAAG CAGAAAGTGA CACTTATGCT GATGGATCAG   1680

GGGTCCTCTC GCCGTCATCT GGGAGATGCG TTCAAGCCTG ACCCCAACAG CAGCAGCTTC   1740

AAGAAACCCA CCGGAGAGAT GAATATCGCC TCTGGCTGCC CAGTCTTTGT CGCCCAAACT   1800

GTTCTAGAGA ACGGGACGTA TATTAAAGAT GATACAATCT TTATTAAGGT CATAGTGGAT   1860

ACCTCGGATC TGCCTGACCC CTGACAAGAA AGCAGGGCGG TGGATTCAGC AGAAGGTAAC   1920

TCCTCTGGGG GGGTGAGCTA GTGTCTTCAC GGAGGTCCTC GCCCTCAGAA AGGACCTTGT   1980

GGCGCAGAGG AAGCAGCCGG AGGAGGAGAA GGAGGTCGAG TGGCTGGCAG GAGAGCCACA   2040

TGTGAAAACA GACCCCAACG GATTTTCTAA TAAACTAGCC ACACCCACTC TGAAGGATTA   2100

TTTATCCATC AACAAGATAA ATACTGCTGT CAGAGAAGGT TTTCATTTTC ATTTTAAAAG   2160

ATCTAGTATT AAGGTGGGAA CATATATGCT AAAAAGAAAC ATGATTTTTC TTCCTTAACT   2220

TAAACACCAA AAAGAGAACA CATGTGGGGG TAGCTGGAGT GTGTACAGTA CCTCGAGGGC   2280

TTAAAATCAT AAACAATCAC ATACTCATCC TAAAATTCAG GGTGCAACTC CGTTTCAAAT   2340

ATTGTATATT GTCTATTTA   2359

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2455 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGGGGAGCG CGGCGCGGCC GCCGCGTGCG CGAGCCGGGG TTGCAGCCCA GCCGGGACTT   60

```
TCCAGCCGGC GGCAGCCGCG GCGGTCGTCG GCTCTTCCCC GCCCCCGTC ATGGGGCAGC     120

CCGGGGAGCA GAACGCTGCG GACCGCGGCG GAGGACGCGC CCGGCGCCCC TGAGCCGGCC     180

GAGCGGCGAC GGACGGCGAG AACTCCTCTT TCCTAAAATG GAGTCGAGTA AAAAGATGGA     240

CTCTCCTGGC GCGCTGCAGA CTAACCCGCC GCTAAAGCTG CACACTGACC GTAGTGCTGG     300

GACGCCAGTT TTTGTCCCTG AACAAGGAGG TTACAAGGAA AAGTTTGTGA AGACCGTGGA     360

GGACAAGTAC AAGTGTGAGA AGTGCCACCT GGTGCTGTGC AGCCCGAAGC AGACCGAGTG     420

TGGGCACCGC TTCTGCGAGA GCTGCATGGC GGCCCTGCTG AGCTCTTCAA GTCCAAAATG     480

TACAGCGTGT CAAGAGAGCA TCGTTAAAGA TAAGGTGTTT AAGGATAATT GCTGCAAGAG     540

AGAAATTCTG GCTCTTCAGA TCTATTGTCG GAATGAAAGC AGAGGTTGTG CAGAGCAGTT     600

AACGCTGGGA CATCTGCTGG TGCATTTAAA AAATGATTGC CATTTTGAAG AACTTCCATG     660

TGTGCGTCCT GACTGCAAAG AAAAGGTCTT GAGGAAAGAC CTGCGAGACC ACGTGGAGAA     720

GGCGTGTAAA TACCGGGAAG CCACATGCAG CCACTGCAAG AGTCAGGTTC CGATGATCGC     780

GCTGCAGAAA CACGAAGACA CCGACTGTCC CTGCGTGGTG GTGTCCTGCC CTCACAAGTG     840

CAGCGTCCAG ACTCTCCTGA GGAGCGAGTT GAGTGCACAC TTGTCAGAGT GTGTCAATGC     900

CCCCAGCACC TGTAGTTTTA AGCGCTATGG CTGCGTTTTT CAGGGACAA ACCAGCAGAT     960

CAAGGCCCAC GAGGCCAGCT CCGCCGTGCA GCACGTCAAC CTGCTGAAGG AGTGGAGCAA    1020

CTCGCTCGAA AAGAAGGTTT CCTTGTTGCA GAATGAAAGT GTAGAAAAAA ACAAGAGCAT    1080

ACAAAGTTTG CACAATCAGA TATGTAGCTT TGAAATTGAA ATTGAGAGAC AAAAGGAAAT    1140

GCTTCGAAAT AATGAATCCA AAATCCTTCA TTTACAGCGA GTGATCGACA GCCAAGCAGA    1200

GAAACTGAAG GAGCTTGACA AGGAGATCCG GCCCTTCCGG CAGAACTGGG AGGAAGCAGA    1260

CAGCATGAAG AGCAGCGTGG AGTCCCTCCA GAACCGCGTG ACCGAGCTGG AGAGCGTGGA    1320

CAAGAGTGCG GGGCAAGTGG CTCGGAACAC AGGCCTGCTG GAGTCCCAGC TGAGCCGGCA    1380

TGACCAGATG CTGAGTGTGC ACGACATCCG CCTAGCCGAC ATGGACCTGC GCTTCCAGGT    1440

CCTGGAGACC GCCAGCTACA ATGGAGTGCT CATCTGGAAG ATTCGCGACT ACAAGCGGCG    1500

GAAGCAGGAG GCCGTCATGG GGAAGACCCT GTCCCTTTAC AGCCAGCCTT TCTACACTGG    1560

TTACTTTGGT TATAAGATGT GTGCCAGGGT CTACCTGAAC GGGGACGGGA TGGGGAAGGG    1620

GACGCACTTG TCGCTGTTTT TTGTCATCAT GCGTGGAGAA TATGATGCCC TGCTTCGTTG    1680

GCCGTTTAAG CAGAAAGTGA CACTCATGCT GATGGATCAG GGGTCCTCTC GACGTCATTT    1740

GGGAGATGCA TTCAAGCCCG ACCCCAACAG CAGCAGCTTC AAGAAGCCCA CTGGAGAGAT    1800
```

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GAATATCGCC TCTGGCTGCC CAGTCTTTGT GGCCCAAACT GTTCTAGAAA ATGGGACATA    1860

TATTAAAGAT GATACAATTT TTATTAAAGT CATAGTGGAT ACTTCGGATC TGCCCGATCC    1920

CTGATAAGTA GCTGGGGAGG TGGATTTAGC AGAAGGCAAC TCCTCTGGGG GATTTGAACC    1980

GGTCTGTCTT CACTGAGGTC CTCGCGCTCA GAAAAGGACC TTGTGAGACG GAGGAAGCGG    2040

CAGAAGGCGG ACGCGTGCCG GCGGGAGGAG CCACGCGTGA GCACACCTGA CACGTTTTAT    2100

AATAGACTAG CCACACTTCA CTCTGAAGAA TTATTTATCC TTCAACAAGA TAAATATTGC    2160

TGTCAGAGAA GGTTTTCATT TTCATTTTTA AAGATCTAGT TAATTAAGGT GGAAAACATA    2220

TATGCTAAAC AAAAGAAACA TGATTTTTCT TCCTTAAACT TGAACACCAA AAAAACACAC    2280

ACACACACAC ACGTGGGGAT AGCTGGACAT GTCAGCATGT TAAGTAAAAG GAGAATTTAT    2340

GAAATAGTAA TGCAATTCTG ATATCTTCTT TCTAAAATTC AAGAGTGCAA TTTTGTTTCA    2400

AATACAGTAT ATTGTCTATT TTTAAGGCCT CCAAAAAAAA AAAAAATTCC GGCCG         2455
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 6 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

    Lys Ala Cys Lys Tyr Arg
    1   5

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant   :   David Baltimore, et al.

Serial No.   :   08/813,323

Filed   :   March 10, 1997   Art Unit: 1815

For   :   TRUNCATED CRAF1 INHIBITS CD40 SIGNALING

> 1185 Avenue of the Americas
> New York, New York 10036
> November 25, 1997

Assistant Commissioner for Patents
Washington, D.C.   20231
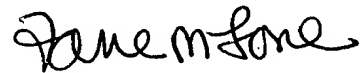
ATTENTION: BOX SEQUENCE

SIR:

STATEMENT IN ACCORDANCE WITH 37 C.F.R. §1.821(f)

In accordance with 37 C.F.R. §1.821(f), I hereby certify that the computer readable form containing the nucleic acid and/or amino acid sequences required by 37 C.F.R. §1.821(f) and submitted in connection with the above-identified application, has the same content as that submitted on pages 40-48 entitled "Sequence Listing," attached hereto as Exhibit B.

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Respectfully submitted,

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